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TCTTBD*E8F2E660

ATATGGCATGGTGTATGGATGTAATTATTAGAAAGCAAAAGCGCTCAATAACT 60
 TATAACCGTACCAACAATACCTACATTATAAATCTTTTCGTTTTCAGCGAGTTATGA

GAGTGGCTTTTTTCTTTGTCTCTCCCTACTGAAAGGAAGTGTCTTACTTGAGTCAA 120
 CTCACCGAAAAAGAAACAGGAGAGGGGATGACTTTCCTTCACTAAGAAATGAACCTCAGTT

Leu Ser Gln
 — Yoml —

AACCTCAAAATTATACTAACCCCGCAAGCTGATACCTCATCCAAAACGTGCGAACAGTTA 180
 TTGGAGTTTTAATATGATTGGGGCGTTCGACTATGGAGTAGGTTTTCACAGCTTGCAAT

Asn Leu Lys Ile Ile Leu Thr Pro Gln Ala Asp Thr Ser Ser Lys Thr Val Glu Gln Leu
 — Yoml —

AATCAGCAAAATTAAATCCCTGGAAAAAGAACTCAACTCCCTCAAGCTCAATACAAACATT 240
 TTAGTCGTTTAAATTAGGGACCTTTCTTTGAGTTGAGGGAGTTCGAGTTATGTTGTAA

Asn Gln Gln Ile Lys Ser Leu Glu Lys Lys Leu Asn Ser Leu Lys Leu Asn Thr Asn Ile
 — Yoml —

FIG. 1A-1

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104180' EBTCE660

GATCTCAACCTTAAAGCCTGCAAGAATCTCCTCTGCTATCGACACATATCAGAAA 300
CTAGATGTTGGAATTTTCGAGCGTTCTTAAGAGGAGACGATAGCTGTGTATAGTCTTT

Asp Ser Thr Thr Leu Lys Ala Leu Gln Glu Phe Ser Ser Ala Ile Asp Thr Tyr Gln Lys
Yomi

AACCTAAATCCTATAATCAACACAGTTAAAGAAAAACCTCAACAGTAATTAAAGAATGCTGAC 360
TTGGATTTTAGGATATTAGTTTGTCAATTTCTTTGGAGTTGTCATTAAATCTTACGACTG

Asn Leu Lys Ser Tyr Asn Gln Thr Val Lys Glu Thr Ser Thr Val Ile Lys Asn Ala Asp
Yomi

GGATCAGTTGAAAAGCTCACCAGCAGTATAAGAAAAAIGGTGAGATACTTCAACGTGAA 420
CCTAGTCAACITTTTCGAGTGGTGCATATTCTTTTACCACCTCATGAAGTTGCACIT

Gly Ser Val Glu Lys Leu Thr Gln Glu Tyr Lys Lys Asn Gly Glu Ile Leu Gln Arg Glu
Yomi

ACAAAAATAATCAACAATCGTAATACAGCATTAAAGCAAGAACTCAAGAGGTTAACAAAG 480
TGTTTTATTAGTTGTTAGCATTATGTCGTAATTTTCGTTCTTTTGAGTCTCCTCAATTGTC

Thr Lys Ile Ile Asn Asn Arg Asn Thr Ala Leu Lys Gln Glu Thr Gln Glu Val Asn Lys
Yomi

FIG._1A-2

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10/180-2872E660

CTACACAGCCCACTGAGAACTAGGACAGGTTCAAAAAAGACTGTGCAGAGAAATCTG 540
 GATTGTCGGGTGACTCTTTGATCCTGTCGAAGTTTTTCTGACACGTCCTCTTAGAC

Leu Thr Gln Ala Thr Glu Lys Leu Gly Gln Val Gln Lys Lys Thr Val Gln Arg Asn Leu
 _____Yoml_____

CAAGACAGCCCAACAAAGGTAGTGCAGAAAAACGCCACGGGTTCGATGATATTTTAT 600
 GTTCTGTCGGTGTTCATCAGCTCTTTTGGCGGTGCCCAAGCTACTATAACAATA

Gln Gly Gln Pro Thr Lys Val Val Gln Lys Asn Arg His Gly Phe Asp Asp Ile Val Tyr
 _____Yoml_____

ACAACGATCCTTAAACTAAATTCGACCTCCTCAAAAACTACAACCTAAATATGACCAACA 660
 TGTGACTAGGATTTTGATTAGCTGGAGGATTTTGTGTTGATTAAATACCTGGTTGTT

Thr Thr Asp Pro Lys Thr Asn Ser Thr Ser Ser Lys Thr Thr Thr Asn Tyr Asp Gln Gln
 _____Yoml_____

AGCAGAGCAATTGACGACCTTAAGCAAGATTTAGAGAAGCTTAGACAGCAAGGATTGTT 720
 TCCCTCGTTAACTCGGATTCGTTCTAAATCTCTTCGAATCTGTCGTTCCATAACAA

Arg Arg Ala Ile Glu Gln Leu Lys Gln Asp Leu Glu Lys Leu Arg Gln Gln Gly Ile Val
 _____Yoml_____

FIG._1B-1

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10/280' EST2E660

ACTGATACGACCATCICATCTCTGGCCGAAAAATAAACACAGCTCAATCCGCTCAACAA 780
 TGACTATGCTGGTAGAGTAGAGAACCCGCTTTTATTGTGTCGAGTTAGCGAGTTGTT

Thr Asp Thr Thr Ile Ser Ser Leu Gly Arg Lys Ile Asn Thr Ala Gln Ser Ala Gln Gln
 _____Yoml_____

ATTGAGCACTGCAAAATAGGATAAGGATGTTAGATGATAAAATCTGCGGCAGTTGCGAAG 840
 TAACTTCGTGACGTTTTATCCTATTCTTACAATCTACTATTTAGACGCCGTCACGCTTC

Ile Glu Ala Leu Gln Asn Arg Ile Arg Met Leu Asp Asp Lys Ser Ala Ala Val Ala Lys
 _____Yoml_____

AACAAAGAAATTAAGAAAAACCATTTGAATTTATATCAGCGACAGGCACCAAGTAAATGTTCAA 900
 TTGTTACTTAATTTCTTTTGGTAACTTAATATAGTCGCTGTCGGTGTTCATTACAAAGTT

Asn Asn Glu Leu Lys Lys Thr Ile Glu Leu Tyr Gln Arg Gln Ala Gln Val Asn Val Gln
 _____Yoml_____

FIG._1B-2

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102180" E812E66D

AACCTAAATACACGGTATGGCAGTTCTATGGGCTCTAGTAATAGACAAGCTGTTCAAGAT
 TTGGATTATGTGCATACCGTCAAGATACCGGAGATCAATTATCTGTTGCGACAAGTTCTA 960

Asn Leu Asn Thr Arg Tyr Gly Ser Ser Met Gly Ser Ser Asn Arg Gln Ala Val Gln Asp
 _____ Yomi _____

TATTTGAATGCAGTAAATAGTCTTAAATGAAGCACTGGAAGCAATAATATCAGATCACAA
 ATAAACTTACGTCATTTATCAGAATTACATTCGTGACCTTCGTTATTATATAGTCTAGTGTT 1020

Tyr Leu Asn Ala Val Asn Ser Leu Asn Val Ser Thr Gly Ser Asn Asn Ile Arg Ser Gln
 _____ Yomi _____

ATTCAAAGCTTGAATATGCAATTTAGAGAATTAGCTTCCAACGCTCAACACAGCTGCTAAT
 TAAGTTTCAACTTATACGTTAAATCTCTTAAATCGGAGGTTGCGAGTTTGTGCGACGATTA 1080

Ile Gln Ser Leu Asn Met Gln Phe Arg Glu Leu Ala Ser Asn Ala Gln Thr Ala Ala Asn
 _____ Yomi _____

CAAGCTCTCTCTTTTGGAGCAGAACTAACCCAAACCTTCAAAAGCATGTCCACCTATTTA
 GTTCGGAGAAGAAAACCTCGTCTTGATTTGGAGTTTTCGTACAGGTGGATAAAT 1140

Gln Ala Ser Ser Phe Gly Ala Glu Leu Thr Gln Thr Phe Lys Ser Met Ser Thr Tyr Leu
 _____ Yomi _____

FIG._1C-1

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T02180* E812E660

ATCTCGGTTCTTTATTCTACGGAGCTATCTCGACITTAAGAAATGGTATCCAGGCA 1200
 TAGAGCCCAAGAAATAAGATGCCCTAGAGAGCCTGAATTTCTTTACCATAGGTCGGT

Ile Ser Gly Ser Leu Phe Tyr Gly Ala Ile Ser Gly Leu Lys Glu Met Val Ser Glu Ala
 _____ Yomi

ATAGAAATIGATACTTCATGACAAATATTCGCCGGTGTATGAATGAGCCGGATTATAAA 1260
 TATCTTTAACTATGAGAGTACTGTTTATAAGCGGCACAAIACCTTACTCGGCCCTAATATTT

Ile Glu Ile Asp Thr Leu Met Thr Asn Ile Arg Arg Val Met Asn Glu Pro Asp Tyr Lys
 _____ Yomi

TATAATGAACCTTCCCAAGAACTATTGACTTAGGTGATACACITTTCAAATAAAATCACAA 1320
 ATATTACTTGAAGAGGTTCTTAGATAACTGAATCCACTATGTGAAAGTTATTTTAGTGT

Tyr Asn Glu Leu Leu Glu Ser Ile Asp Leu Gly Asp Thr Leu Ser Asn Lys Ile Thr
 _____ Yomi

GATATTCTCAAATGACAGCGCATTTTGGGAGAATGGGTTTCGATGAAAGTGAGCTCTCC 1380
 CTATAAGAAGTTTACTGTCCGCTAAACCCCTCTTACCCAAAGCTACTTTCACCTCGAGAGG

Asp Ile Leu Glu Met Thr Gly Asp Phe Gly Arg Met Gly Phe Asp Glu Ser Glu Leu Ser
 _____ Yomi

FIG. 1C-2

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POLYBUTADIENE

ACGTTAACGAAAACTGCCAAGTTCTTCAAAATGTCTCTGATTAACTCCCGATGATACA
 TGC AATTGCTTTTGTACGGGTTCAAGAAGTTTACAGAGACTAAATTTAGGGCTACTATGT

1440

Thr Leu Thr Lys Thr Ala Gln Val Leu Gln Asn Val Ser Asp Leu Thr Pro Asp Asp Thr
 Yomi

GTTAACACTCTAACGSCCAATGCTCAACTTAAATATTGCAGCAAAATGATTCAAATACA
 CAATTGTGAGATTGCCGTCGTTACGAGTTGAAATTATAACGTCGTTTACTAAGTTATAGT

1500

Val Asn Thr Leu Thr Ala Ala Met Leu Asn Phe Asn Ile Ala Ala Asn Asp Ser Ile Ser
 Yomi

ATTGCAGATAAATTAAATGAGGTTGATAATAACTATGCTGTTACAACTCTAGATCTGGCC
 TAACGCTATTAAATTACTCCAACATAATTGATACGACAAATGTTGAGATCTAGACCGG

1560

Ile Ala Asp Lys Leu Asn Glu Val Asp Asn Asn Tyr Ala Val Thr Leu Asp Leu Ala
 Yomi

AATTCTATCCGTAAGCTGGTTCAACTGCTTCTACATTTCGGGGTAGAGCTAAATGATCTT
 TTAAGATAGGCATTTTCGACCAAGTTGACGAAGATGAAGCCCCATCTCGATTTACTAGAA

1620

Asn Ser Ile Arg Lys Ala Gly Ser Thr Ala Ser Thr Phe Gly Val Glu Leu Asn Asp Leu
 Yomi

FIG. 1D-1

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702180' 88125600

ATGGTTATACAACTGCAATTGCTAGTACAAACACGIGAAATCAGGGAATATCGTCGGGAAC
 TAACCAATATGTTGACGTTAACGATCATGTTGTGCACCTAGTCCCTTATACGACCCCTTG
 1680

Ile Gly Tyr Thr Ala Ile Ala Ser Thr Thr Arg Glu Ser Gly Asn Ile Val Gly Asn
 Yoml

TCCTTAAGACAAATTTTCGCGCGGATTGGGAATAATCAAAGCTCAATTAAGCGTTAGAA
 AGGAATTTCTGTAAAGCGCGCTAACCCCTATTAGTTTCGAGTTAAATTCGCAATCTT
 1740

Ser Leu Lys Thr Ile Phe Ala Arg Ile Gly Asn Asn Gln Ser Ser Ile Lys Ala Leu Glu
 Yoml

CAGATTGGTATCTCAGTTAAACAGCTGGTGGTGAAGCTAAATCAGCAAGTGATTTAATT
 GTCTAACCATAGAGTCAATTTTGTGACACCACCCTTCGATTIAGTCGTTCACTAAATTA
 1800

Gln Ile Gly Ile Ser Val Lys Thr Ala Gly Gly Glu Ala Lys Ser Ala Ser Asp Leu Ile
 Yoml

AGTGAGTTGCTGGTAAGTGGGATACGCTTCTGTATGCTCAGAAACAAAATACTTCAATT
 TCACCTCAACGACCAATTCACCCCTATGCGAAGACTACGAGCTTTGTGTTTATGAAGTTAA
 1860

Ser Glu Val Ala Gly Lys Trp Asp Thr Leu Ser Asp Ala Gln Lys Gln Asn Thr Ser Ile
 Yoml

FIG. 1D-2

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F02T80'2812E660

GGAGTAGCTGGTATTATCAATTATCCGTTTTAATGCAATGATGAACAATCTCTATT
 CCTCATGCACCAATAAATAGTTAATAGGCCAAAATTACGTTACTACTTGTTGAAGAGATAA
 1920
 Gly Val Ala Gly Ile Tyr Gln Leu Ser Arg Phe Asn Ala Met Met Asn Phe Ser Ile
 Yoml
 GCTCAGAATGCGGCTAAAACTGCGGCTAACTCAACAGGAAGTGCTTGGAGTGAAGCAGCAA
 1980
 CGAGTCTTACGCCGATTTTGACGCCGATTGAGTTGCTCTTCACGAACCTCAGTCGCTT
 Ala Gln Asn Ala Ala Lys Thr Ala Ala Asn Ser Thr Gly Ser Ala Trp Ser Gln Gln
 Yoml
 AAGTATGCAGATAGTCTACAAGCTAGGTTAAATAAGCTTCAAAATAACTTCACTGAATTT
 2040
 TTATACGCTATCAGATGTCGATCCCATTTATTCGAAGTTTATTGAAGTGACTTAAA
 Lys Tyr Ala Asp Ser Leu Gln Ala Arg Val Asn Lys Leu Gln Asn Asn Phe Thr Gln Phe
 Yoml
 GCTATTGCAGCTTCTGATGCTTTTATTAGCGACGGATTAAATGAATTTACTCAAGCCGCA
 2100
 CGATAACGTCGAGACTACGAAAATAATCGCTGCTAATTAACTTAAATGAGTTCGGCGT
 Ala Ile Ala Ala Ser Asp Ala Phe Ile Ser Asp Gly Leu Ile Gln Phe Thr Gln Ala Ala
 Yoml

FIG. 1E-1

10/31

T02180" E812E660

GGTCTTTGCTTAACGCTTCTACAGGAGTAATCAATCAGTTGGTTTCTTACCTCCCTT
 CCAAGAACGAATTCGAAGATGCTCTCATTAGTTAGTCAACCCCAAGGATGGAGGGAA 2160

Gly Ser Leu Leu Asn Ala Ser Thr Gly Val Ile Lys Ser Val Gly Phe Leu Pro Pro Leu
 Yomi

TTAGCTGCAGTAAGCACATGCAACCCCTTTTGCTCAGTAAGAATACCCGCACATTAGCAGC
 AATCGACGTCATTGCTGACGTTGGGAAAACGAGTCATTCTTATGGGCGTGAATCGGTCG 2220

Leu Ala Ala Val Ser Thr Ala Thr Leu Leu Ser Lys Asn Thr Arg Thr Leu Ala Ser
 Yomi

AGCCTAATTTTGGGCACACGTCGCAATGGGGCAAGAACTTTAGCGACTGCTGGGCTAGAA
 TCGGATTAAACCCGCTGTGCAGTTACCCCGTTCTTTGAAATCGCTGACGACCCGATCTT 2280

Ser Leu Ile Leu Gly Thr Arg Ala Met Gly Gln Glu Thr Leu Ala Thr Ala Gly Leu Glu
 Yomi

GCCTGATGACTCGTCGACGAGTCGCCCTCAAGAGTTCTAAAAACTGCTCTTCGAGGGTTG
 CGACCATACTGACACGTCGTCAGCGAGTTCTCAAGATTTTGTACGAGAAGCTCCCAAC 2340

Ala Gly Met Thr Arg Ala Ala Val Ala Ser Arg Val Leu Lys Thr Ala Leu Arg Gly Leu
 Yomi

FIG. 1E-2

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104180-EST2E660

CTGTTCACCTTAGTTGGCGTGCAATTGCTGCTTTGGGATGGCGCTAGAAATCATTA 2400
 GAACAAAGTTGAATCAACGCCACGTAACGACGAAACCCTACCCGCGATCTTAGTAAT

Leu Val Ser Thr Leu Val Gly Ala Phe Ala Leu Gly Trp Ala Leu Glu Ser Leu
 _____Yoml_____

ATTCTTCTTTTGCAGAAGCTAAAAAGCTAAAGATGATTTTGAGCAGAGCCAGCAAAACC 2460
 TAAAGAGAAAAACGCTTCGATTTTTCGATTTCTACTAAAACTCGTCGGTCGTTTGG

Ile Ser Ser Phe Ala Glu Ala Lys Lys Ala Lys Asp Asp Phe Glu Gln Ser Gln Thr
 _____Yoml_____

AATGCGAAGCAATTACGACCAATAAAGACTCCACTGATATAACTAATACAGCAATATAAA 2520
 TTACAGCTTCGTTAATGCTGGTATTCTCGAGGTGACTATTGATTATGTCGTTATATT

Asn Val Glu Ala Ile Thr Thr Asn Lys Asp Ser Thr Asp Lys Leu Ile Gln Gln Tyr Lys
 _____Yoml_____

GAGCTTCAAAAAGTTAAAGAGTCAAGATCTTTAACTTCAGATGAAGCAAGAATACCTT 2580
 CTCGAAGTTTTTCAATTCTCAGTCTAGAAATTGAAGTCTACTTCTCGTTCTTATGGAA

Glu Leu Gln Lys Val Lys Glu Ser Arg Ser Leu Thr Ser Asp Glu Glu Gln Tyr Leu
 _____Yoml_____

FIG.-1F-1

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FD4180-EB12E660

CAAGTCACTCAGCAATTAGCACAAACTTTCCCTGCATTAGTTAAAGGCTATGATTTCTCAA 2640
 GTTCAGTGAGTCGTTAATCGTGTTTGAAAGGGACGTAATCAATTTCCGATACTAAGAGTT

Gln Val Thr Gln Gln Leu Ala Gln Thr Phe Pro Ala Leu Val Lys Gly Tyr Asp Ser Gln
 _____Yomi_____

GGAAATGCAATTCTTAAGACAAATAAGAGCGTTTGAAAAAGCGATTGAGATACTAAAGAG 2700
 CCTTTACGTTAAGAATTCTGTTTATTCTCGAACTTTTTCGCTAACTCTTAAGATTTCTC

Gly Asn Ala Ile Leu Lys Thr Asn Lys Glu Leu Glu Lys Ala Ile Glu Asn Thr Lys Lys
 _____Yomi_____

TATTGGCTTTAAAGAAACAAGAACAGAGACAGCGCAAGAAAAACATTCGAAGACGCT 2760
 ATAAACCGAAATTTCTTTGTTCTCTGTCGCGTTTCTTTTGTAAGCTTCTGCGA

Tyr Leu Ala Leu Lys Lys Gln Thr Arg Asp Ser Ala Lys Lys Thr Phe Glu Asp Ala
 _____Yomi_____

ICTAAGGAATTAAGGCTAAGGATGAATTAAGCAGTACAACAAATAGCTGACTAC 2820
 AGATTCTTTAAITTTTCAGATTCTACTTAATTCGTCATGTTTGTTATCGACTGATG

Ser Lys Glu Ile Lys Lys Ser Lys Asp Glu Leu Lys Gln Tyr Lys Gln Ile Ala Asp Tyr
 _____Yomi_____

FIG.. 1F-2

13 / 31

102780-88128660

AACGATAAGGTAGACCTAAATGGGATCTCATTCCAGATGACGATGACTATAAGGTTGCA
 TTGCTATTTCCATCTGGATTTACCCTAGAGTAGGCTCTACTGCTACTGATATATCCAACGT 2880

Asn Asp Lys Gly Arg Pro Lys Trp Asp Leu Ile Ala Asp Asp Asp Tyr Lys Val Ala
 _____Yomi_____

GCTGATAAAGCTAAACAAAGTATGCTCAAAAGCTCAATCTGACATTGAGAGTGGAAATGCT
 CGACTATTTTCGATTTGTTTCATACGAGTTTCGAGTTAGACTGTAACCTCACCCTTACGA 2940

Ala Asp Lys Ala Lys Gln Ser Met Leu Lys Ala Gln Ser Asp Ile Glu Ser Gly Asn Ala
 _____Yomi_____

AAAGTTAAAGATAGCGTCCTTTCAATTGCAAAIGCTTATAGTTCAATTGATATCAGTAAT
 TTTCAAATTTCTATCGCAGAAAGTTAAGGTTACGAATATCAAGTTAACTATAGTCATTA 3000

Lys Val Lys Asp Ser Val Leu Ser Ile Ala Asn Ala Tyr Ser Ser Ile Asp Ile Ser Asn
 _____Yomi_____

ACTTTAAAGACGAGTATTAGTGATGTTGTCAACAAACCTTAAAGATGATTTAGAT
 TGAAATTTCTGCTCATATAATCACTACACACAGTTGTTGAATTGAATTTTCTACTAAATCTA 3060

Thr Leu Lys Thr Ser Ile Ser Asp Val Val Asn Lys Leu Asn Leu Lys Asp Asp Leu Asp
 _____Yomi_____

FIG._1G-1

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FOUO-2812660

CCTGAAGAATTAGAAAAATTCCTCTCTTTAGGAAAGCTTCAAGAAAAATGCAAAA 3120
 GGACTTCTTAATCTTTTAGAGAGAGAAATCCTTTCGAAGTCTTTTACGTTTTT

Pro Glu Glu Leu Glu Lys Phe Ser Ser Ser Leu Gly Lys Leu Glu Glu Lys Met Gln Lys
 _____Yoml_____

GCTTTAGATTACGGCGATGAAAAAGCTTTCGATAACGCCAAAAAAGATCTTCAAGTCTC 3180
 CGAAATCTAAGTCGCGTACTTTTCGAAAGCTATTGCGTTTTTTCTAGAAGTTTCAGAG

Ala Leu Asp Ser Gly Asp Glu Lys Ala Phe Asp Asn Ala Lys Lys Asp Leu Gln Ser Leu
 _____Yoml_____

TGGAAACATACTCCAAATCCGATTCCTCTATTGATGTTTTTAAAAATGAGCTTCGACAA 3240
 AACCTTGTATGAGGTTTAGGCTAGAAGATAACTACAAAAATTTTACTCGAAGCTGTTT

Leu Glu Thr Tyr Ser Lys Ser Asp Ser Ser Ile Asp Val Phe Lys Met Ser Phe Asp Lys
 _____Yoml_____

GCACAGAAGAACATAAAGATGGAGATAAGAGCTTATCTCCGTCAAACTGAAGTTGGT 3300
 CGTGCTCTCTGTATTTTCTACCTCTATTCTCGAATAGAAGGCAGTTTAGACTTCAACCA

Ala Gln Lys Asn Ile Lys Asp Gly Asp Lys Ser Ser Leu Ser Ser Val Lys Ser Glu Val Gly
 _____Yoml_____

FIG. 1G-2

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102180-8812E660

GATTAGGTGAGCGCTGGCAGAGCAGGTAAACGAGGCAGAACATTTGGTAAGAAGCTA
 CTAATCCACTTCGACCGCTTCGTCCATTGCTCCGCTTCTAAACCATTTCTTCGAT
 3360

Asp Leu Gly Glu Thr Leu Ala Glu Ala Gly Asn Glu Ala Glu Asp Phe Gly Lys Lys Leu
 Yomi

AAAGAAGCTCTGGATGCAAAATAGTGTGATGATATTAAAGGCAGCTATTAAAGAAATGTCA
 TTTCTCGAGACCTACGTTTATCACAACTACTATAATTCCGTCGATAATTTCTTTACAGT
 3420

Lys Glu Ala Leu Asp Ala Asn Ser Val Asp Asp Ile Lys Ala Ala Ile Lys Glu Met Ser
 Yomi

GATGCTATGCAGTTCGATTCCGTTCAAGATGCTTAAATGGGGATATTTTAAATAACACC
 CTACGATACGTCAAGCTAAGGCAAGTCTACAGAAATTACCCCTATAAAAAATTATTGTGG
 3480

Asp Ala Met Gln Phe Asp Ser Val Gln Asp Val Leu Asn Gly Asp Ile Phe Asn Asn Thr
 Yomi

AAAGATCAAGTAGCTCCTCTCAATGATCTTCTGGAAAAAATGGCTGAAGGTAAAAGTATT
 TTCTAGTTTCATCGAGGAGAGTTACTAGAGACCTTTTACCAGACTTCCATTTTCATAA
 3540

Lys Asp Gln Val Ala Pro Leu Asn Asp Leu Glu Lys Met Ala Glu Gly Lys Ser Ile
 Yomi

FIG. 1H-1

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P02180-ES123660

ICTGCAATGAAGCTAATACCCTTATTCAAAGATAAGGAAGTGGCCAGGCTATTAGC
 +-----+-----+-----+-----+-----+-----+-----+-----+
 AGACGTTTACCTTCGATTATGGAATAAGTTTTCTATTCCCTTGAACGGGTCGATAATCG
 +-----+-----+-----+-----+-----+-----+-----+-----+ 3600

Ser Ala Asn Glu Ala Asn Thr Leu Ile Gln Lys Asp Lys Glu Leu Ala Gln Ala Ile Ser
 -----Yomi-----

ATGAAAATGGCGTTGTGAAAATTACCGTGATGAAGTTATCAACAAGAAAGTTAAA
 +-----+-----+-----+-----+-----+-----+-----+-----+
 TAGCTTTTACCGCAACACATTTTAATTGGCACACTTCAATAGTTTCTTTTCAATTT
 +-----+-----+-----+-----+-----+-----+-----+-----+ 3660

Ile Glu Asn Gly Val Val Lys Ile Asn Arg Asp Glu Val Ile Lys Gln Arg Lys Val Lys
 -----Yomi-----

CTTGATGCTTATACGACATGGTTACCTACAGCAATAAATTGATGAAAACAGAAGTTAAC
 +-----+-----+-----+-----+-----+-----+-----+-----+
 GAACTACGAATATTGCTGTACCAATGGATGTCGTTATTAACTACTTTTGTCTTCAATTG
 +-----+-----+-----+-----+-----+-----+-----+-----+ 3720

Leu Asp Ala Tyr Asn Asp Met Val Thr Tyr Ser Asn Lys Leu Met Lys Thr Glu Val Asn
 -----Yomi-----

AAGCTATCAAAAACTTTAAACGCTGATACCTTACGGATTGACAGCCTGAAAAGCTACGA
 +-----+-----+-----+-----+-----+-----+-----+-----+
 TTGCGATAGTTTGAATAATTCCGACTATGGAATGCCTAACGTCTCGGACTTTTTCGATGCT
 +-----+-----+-----+-----+-----+-----+-----+-----+ 3780

Asn Ala Ile Lys Thr Leu Asn Ala Asp Thr Leu Arg Ile Asp Ser Leu Lys Lys Leu Arg
 -----Yomi-----

FIG. 1H-2

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Y02F80-88F2E660

AAAGAACGAAAGCTTGATATGCTGAGGCCGAACCTGTCAGACCTAGAGTTAAGTCAATT
 TTCTTGCTTTCGAACATACAGACTCCGGCTTGACAGTCTGGATCTTCAATTCAGTTAA 3840

Lys Glu Arg Lys Leu Asp Met Ser Glu Ala Glu Leu Ser Asp Leu Glu Val Lys Ser Ile
 _____Yomi_____

AATAATGTTGCAGATGCAAAAAAGAACTTAAAAAGCTTGAGAGAAAAATGCTTCAACCT
 TTATTACAACGCTACGTTTTTTTCTTGAATTTTTCGAACCTCTCTTTACGAAGTTGGA 3900

Asn Asn Val Ala Asp Ala Lys Lys Glu Leu Lys Lys Leu Glu Glu Lys Met Leu Gln Pro
 _____Yomi_____

GGTGGATACTCCAATAGTCAAAATTGAAGCAATGCAAGCGTTAAATCAGCTTTAGAAATCT
 CCACCTATGAGGTTATCAGTTAACTTCGTTACGTTTCGCAATTGATCGAAATCTTAGA 3960

Gly Gly Tyr Ser Asn Ser Gln Ile Glu Ala Met Gln Ser Val Lys Ser Ala Leu Glu Ser
 _____Yomi_____

TATATTTCTGCACTGAGAAGCCACCAGTACACAGAAATGAATAAACAGGCACCTTGTT
 ATATAAGACGTAGACTTCTCGGTGGTCACTGCTCTTTACTTATTGTCGCGTAACAA 4020

Tyr Ile Ser Ala Ser Glu Glu Ala Thr Ser Thr Gln Glu Met Asn Lys Gln Ala Leu Val
 _____Yomi_____

FIG. 11-1

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PCT/US98/18828

GAAGCTGGAACATCATTTGGAGAATTGGACAGATCAACAGAAAAAGCAATGAAGAAACC
 4080
 CTTCGACCTGTAGTAACCTCTTAACCTGTCTAGTTGTTCTTTTCGGTTACTCTTTTGG

Glu Ala Gly Thr Ser Leu Glu Asn Trp Thr Asp Gln Gln Glu Lys Ala Asn Glu Glu Thr
 _____Yomi_____

AAGACTTCCATGTATGTTGTATATAAATACAAGGAGCAATTAGAAAAAGTTAATGCTGAG
 4140
 TTCTGAAGGTACATACAACAACCTATTATGTTCTTCGTAATCTTTTCAATTACGACTC

Lys Thr Ser Met Tyr Val Val Asp Lys Tyr Lys Glu Ala Leu Glu Lys Val Asn Ala Glu
 _____Yomi_____

ATTGACAAGTACACAAGCAGGTCATGATTATCCTAAATACTCTCAGAAATATCGAGAT
 4200
 TAAC TGTTTCATGTTGTTCTGCCAGTTACTAATAGGATTTATGAGAGCTTTTATAGCTCTA

Ile Asp Lys Tyr Asn Lys Gln Val Asn Asp Tyr Pro Lys Tyr Ser Gln Lys Tyr Arg Asp
 _____Yomi_____

GCAATCAAGAAGAANAATTAAAGCAGCTTCAGCAAAAAGAAAAAGCTTATGAGGAACAAGCT
 4260
 CGTAGTCTTCTTCTTAATTTCGTAAGTCGTTTCTTTTCGAAATAGCTCTCTGTTGTCGA

Ala Ile Lys Lys Glu Ile Lys Ala Leu Gln Gln Lys Lys Lys Leu Met Gln Glu Glu Ala
 _____Yomi_____

FIG. 11-2

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TGCATGCTTAAAGATCAAAATTAATCCGGTAACATTACTCAATACGGTATTGTAACCTCT

AAGCTGCTTAAAGATCAAAATTAATCCGGTAACATTACTCAATACGGTATTGTAACCTCT
 TCGACGAATTTCTAGTTTAATTAGGCCATTGTAATGAGTTATGCCATAACATTGGAGA
 4320

Lys Leu Leu Lys Asp Gln Ile Lys Ser Gly Asn Ile Thr Gln Tyr Gly Ile Val Thr Ser
 Yomi

ACAACTTCTTCTGGTGGAAACCCCTCTCAACTGGTGGATCATATTCAGGCAAGTATTCA
 TGTGAGAAGACCACCTTTGGGGAGGAGTTGACCACCTAGTATAGTCCGTTTCATAAGT
 4380

Thr Thr Ser Ser Gly Gly Thr Pro Ser Ser Thr Gly Gly Ser Tyr Ser Gly Lys Tyr Ser
 Yomi

AGCTACATAAATTCAGCAGCTAGTAAATACAATGTTGACCCCTGCCCTTATTGCAAGTGT
 TCGATGTATTTAAGTCGTCGATCATTTTATGTTACAACCTGGGACGGGAATAACGTCGACAT
 4440

Ser Tyr Ile Asn Ser Ala Ala Ser Lys Tyr Asn Val Asp Pro Ala Leu Ile Ala Ala Val
 Yomi

ATTACGACGAATTCAGGGTTTAATGCTAAAGCACCAGTCTGGTGTAGTGCCATGGGATTA
 TAAGTCGTTCTTAGTCCCAAATTACGATTTCGTCTAGACCACATCCACGGTACCCTAAT
 4500

Ile Gln Gln Glu Ser Gly Phe Asn Ala Lys Ala Arg Ser Gly Val Gly Ala Met Gly Leu
 Yomi

FIG._1J-1

20/31

F02F80-EST2E660

ATGCAACTGATGCCAGCACAGCAAAAGCTTAGGAGTAAATAACGCTTACGATCCTTAT
 TAGGTTGACTACGGTCGTTGCTGTTTTTCGAATCCTCATTATTGCGAATGCTAGGAATA 4560

Met Gln Leu Met Pro Ala Thr Ala Lys Ser Leu Gly Val Asn Asn Ala Tyr Asp Pro Tyr
 Yomi

CAAAATGTTATGGGTGGAACAAGTACCTCGCCCAACAACCTTGAAAAGTTTGGCGGTAAT
 GTTTTACAATACCCACCTTGTTCATGGAGCGGGTTGTTGAACTTTTCAAACCGCCATT 4620

Gln Asn Val Met Gly Thr Lys Tyr Leu Ala Gln Gln Leu Glu Lys Phe Gly Gly Asn
 Yomi

GTTGAAAAGCATTGGCTGCATATAATGCTGGGCCCTGGTAACGTAATTAAATATGGTGGT
 CAACTTTTTCGTAAACCGACGTATATTACGACCGGACCATTGTCATTAAATTTATACCACT 4680

Val Glu Lys Ala Leu Ala Ala Tyr Asn Ala Gly Pro Gly Asn Val Ile Lys Tyr Gly Gly
 Yomi

ATCCCTCCTTTTAAAGAAACACAGAAATTACGTCAGAAGATCATGGCCAACATATAGCAAA
 TAGGGAGGAAAATTTCTTTGGTGCTTAATGCAGTTCCTCTAGTACCGGTTGATATCGTTT 4740

Ile Pro Pro Phe Lys Glu Thr Gln Asn Tyr Val Lys Lys Ile Met Ala Asn Tyr Ser Lys
 Yomi

FIG._1J-2

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YDCTBD-28125660

TCGCTCATCTGCCACTTCTTCAATCGCAGCTATTATACAAATAATAGCCCTTTAGG 4800
 AGCGAGAGTAGACGGTGAAGAAGTTAGCGGTGCGATAATATGTTTATTATCGCGAAATCC

Ser Leu Ser Ser Ala Thr Ser Ser Ile Ala Ser Tyr Tyr Thr Asn Ser Ala Phe Arg
 _____Yomi_____

GTAAGTCCAAATATGACAAACAGGAATCTGGTCTCCGCTCCTCCCCACACAAAGGAAT 4860
 CATTGAGGTTTATACCTGTGTCTTAGACCAGAGGGCGAGGGGTGTGTTTCCTTGA

Val Ser Ser Lys Tyr Gly Gln Gln Ser Gly Leu Arg Ser Ser Pro His Lys Gly Thr
 _____Yomi_____

GATTTGCTGCAAAAGCAGGTACAGCAATTAATCTCTTCAAGTGGTAAAGTCCAAT 4920
 CTAACACACGTTTTTCGTCCTGTCGTTAATTTAGAGAGTTTCACCATTTTCAGGTTAA

Asp Phe Ala Ala Lys Ala Gly Thr Ala Ile Lys Ser Leu Gln Ser Gly Lys Val Gln Ile
 _____Yomi_____

GCTGGCTACAGTAAACTGCAGGTAACTGGGTTGTTATTAAACAGGATGATGGAACAGTT 4980
 CGACCGATGTCATTTTGACGTCCATTGACCCCAACAATAATTTGCTCTACTACCTTGTCAA

Ala Gly Tyr Ser Lys Thr Ala Gly Asn Trp Val Val Ile Lys Gln Asp Asp Gly Thr Val
 _____Yomi_____

FIG. 1K-1

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FD2780.E812E66D

GCCAAGTACATGCATTAACACICTCTCTGTAAGCAGGTCAATCAGTTAAAGCC
 CGGTTTCATGTACGATGTGAGGAAGACATTTTCGTCCAGTTAGTCAATTTCCG 5040

Ala Lys Tyr Met His Met Leu Asn Thr Pro Ser Val Lys Ala Gly Gln Ser Val Lys Ala
 _____Yoml_____

GGTCAAACTATTGGTAAAGTTGGTAGTACAGGGAACTCGACTGGGAACCACTTTCATTTA
 CCAGTTTGATAACCAATTTCAACCATCATGTCCTTGAGCTGACCCCTTGGTGGAAAGTAAAT 5100

Gly Gln Thr Ile Gly Lys Val Gly Ser Thr Gly Asn Ser Thr Gly Asn His Leu His Leu
 _____Yoml_____

CAGATCGAACAATAATGGAAAAACAATCGATCCTGAAAAAGTACATGCAAGGATTTGGAAC
 GCTAGCTGTGTTTACCTTTTGTAGCTAGGACTTTTCATGTAGCTTCCATAACCTTGA 5160

Gln Ile Glu Gln Asn Gly Lys Thr Ile Asp Pro Glu Lys Tyr Met Gln Gly Ile Gly Thr
 _____Yoml_____

TCTATTTTCAGATGCGTCACAAGCTGAGGCAGACGACACAAAGGATAGCTCAGGCTAAA
 AGATAAGTCTACGACGATTCGACTCCGCTTGCCTGTTGTTCCCTATCGAGTCCGATTT 5220

Ser Ile Ser Asp Ala Ser Gln Ala Glu Ala Glu Arg Gln Gln Gly Ile Ala Gln Ala Lys
 _____Yoml_____

FIG. 1K-2

23 / 31

Y0180*E8122660

TCTGATCTTCTCCCTCCAGGAGATATCAGTTCAGTCAATGATCAGATTCAAGAATT
 AGACTAGAGAGAGGGAGGTTCTCTATAGTCAAGTCAGTACTAGTCTAAGTCTTGAA 5280

Ser Asp Leu Leu Ser Leu Gln Gly Asp Ile Ser Ser Val Asn Asp Gln Ile Gln Glu Leu
 _____Yomi_____

CAGTATGAAGTACTTCAATCTAACTCGATGAGTTTGATAAAGAATTGGAGATTTTGAT
 GTCATACTTGATCAAGTTAGATTGAGCTACTCAAACTATTTTCTTAACCTCTAAAACTA 5340

Gln Tyr Glu Leu Val Gln Ser Lys Ser Lys Leu Asp Glu Phe Asp Lys Arg Ile Gly Asp Phe Asp
 _____Yomi_____

GTTCGGATAGCAAAAGATGAGTCAATGGCTAACAGATACACTTCTGACAGCAAGGAATTC
 CAAGCCTATCGTTTCTACTCAGTTACCGATTGTCTATGTGAAGACTGTCGTTCTCTAAG 5400

Val Arg Ile Ala Lys Asp Glu Ser Met Ala Asn Arg Tyr Thr Ser Asp Ser Lys Glu Phe
 _____Yomi_____

CGAAATATACCTCTGATCAGAAAAAGCTGTGGCAGAGCAAGCTAAATCCCAACAACAA
 GCTTTTATGTGGAGACTAGTCTTTTTCACACCGTCTCGTTCGATTTTAGGTTGTTGT 5460

Arg Lys Tyr Thr Ser Asp Gln Lys Lys Ala Val Ala Glu Gln Ala Lys Ile Gln Gln Gln
 _____Yomi_____

FIG._1L-1

24 / 31

T02180-5812660

AAAGTTAATTGGATTCAAAAAGAAATTAAACAAATAAAGCAATTGAACCTCGCTCAACGT 5520
 TTTCAATAACCTAAGTTTTTCTTTAATTTTGTTTATTTTCGTAACTTGAGCGGAGTTGCA

Lys Val Asn Trp Ile Gln Lys Glu Ile Lys Thr Asn Lys Ala Leu Asn Ser Ala Gln Arg
 _____Yomi_____

GCACAGCTTCAAGAAGAGCTTAAACAGGCCAAGCTAGATTTAATTTCTGTTCAAGACCAG 5580
 CGTGCGAAGTTCTCTCGAATTTGTCCGGTTCGATCTAAATTTAAAGACAAAGTTCTGGTC

Ala Gln Leu Gln Glu Leu Lys Lys Gln Ala Lys Leu Asp Leu Ile Ser Val Gln Asp Gln
 _____Yomi_____

GTTCGTGAGCTACAGAAACAACCTTGTTCAATCTAAAGTTGATGAGACACTTAAAGTCAATT 5640
 CAGCACTCGATGCTTTGTTGAACAAGTTAGATTTCAACTACTCTGTGAATTCAGTTAA

Val Arg Glu Leu Gln Lys Gln Leu Val Gln Ser Lys Val Asp Glu Thr Leu Lys Ser Ile
 _____Yomi_____

GAAAAGTCATCTTCTAAACCCCAAGGGAATAAAGATGTCGATAACAAAAATTTCAATG 5700
 CTTTTCAGTAGAAGATTTGGGTTCCCTTTTAATTTCTACAGCTATTGTTTAAAGTTAC

Glu Lys Ser Ser Ser Lys Thr Gln Gly Lys Ile Lys Asp Val Asp Asn Lys Ile Ser Met
 _____Yomi_____

FIG. 1L-2

25 / 31

T02180' 28722660

ACTGAAGAAGATGAAGACAAGTTAAATACTATAGCAAGCAATAAAGCTCATTTCAACAA
 5760
 TGACTTCTTCTACTCTGTTCCAATTTATGATATCGTTTCGTTTATTTCGAGTAAGTTGTT

Thr Glu Glu Asp Glu Asp Lys Val Lys Tyr Tyr Ser Lys Gln Ile Lys Leu Ile Gln Lys
 Yomi

CAACAAAAGGAAGCGAAGAAATACATTAGCAGCTTGAGAACAAAGAAAGCTGCGAAA
 5820
 GTTGTTCCTTCGCTTCTTTATGTAATTCGTCGAACCTTCGTTCCTTCGACGCTTT

Gln Gln Lys Glu Ala Lys Lys Tyr Ile Lys Lys Gln Leu Glu Gln Lys Lys Ala Ala Lys
 Yomi

GGTTTCCTGACATCCAGGAACAGATCACATGAAGAAATGCAAACTGGAAGATAAACAG
 5880
 CCAAGGGACTGTAGGTCTTGTCTAGTACTTCTTACGTTTTCGACCTTCTATTGTC

Gly Phe Pro Asp Ile Gln Glu Gln Ile Thr Glu Glu Met Gln Asn Trp Lys Asp Lys Gln
 Yomi

AAAGATTTTAACCTTGAGCTTTATAACACCAAGAAAGTCGATCAAGGATATCTATAAATCA
 5940
 TTCTAAAATTGGAACTCGAAATATGTGGTTCTTCAGCTAGTTCCTATAGATATTAGT

Lys Asp Phe Asn Leu Glu Leu Tyr Asn Thr Lys Lys Ser Ile Lys Asp Ile Tyr Lys Ser
 Yomi

FIG. 1M-1

26 / 31

Y0180" E8F2E660

TTGGCTGATGAAGTTGTATCCATCTACAAAGAGATGTACAAAAATCGTGATATTGAG
 AACCGACTACTTCAACATAGTAGATGTTCTCTACATGCTTTTTTACGCACTATACTC
 6000

Leu Ala Asp Glu Val Val Ser Ile Tyr Lys Glu Met Tyr Glu Lys Met Arg Asp Ile Glu
 Yomi

TTAGAAGCGCATCAGAAAGCGACTCAAGACTTTGATCGATGAGATAGACAAGACTGATGAC
 AATCTCGCGTAGTCTTTTCGCTGAGTTCTGAACTAGCTACTCTATCTGTTCTGACTACTG
 6060

Leu Glu Ala His Gln Lys Ala Thr Gln Asp Leu Ile Asp Glu Ile Asp Lys Thr Asp Asp
 Yomi

GAGGCTAAATTTCAAAAAGAAATTAAGAAGACAAAGACAGTATTTCAAAAGTTGACTGAC
 CTCGGATTAAAGTTTTTCTTAATTTCTTCTGTTCTGTCATAAGTTTCAACTGACTG
 6120

Glu Ala Lys Phe Gln Lys Glu Leu Lys Glu Arg Gln Asp Ser Ile Gln Lys Leu Thr Asp
 Yomi

CAAAATTAATCAATACTCTTTGATGATTTCTGAATTCGGAAGTCAAAAGTCAAAAGACTA
 GTTTAATTAGTATGAGAGAACTACTAAGACTTAAGCCTTTTCAGTTTTCAGTTTCTTGAT
 6180

Gln Ile Asn Gln Tyr Ser Leu Asp Asp Ser Glu Phe Gly Lys Ser Lys Val Lys Glu Leu
 Yomi

FIG. 1M-2

27 / 31

102180-28722660

ACTGAACAGCTTCAAAAAGAGCAGTTAGACCTTGATGATTTTCTAAAGGATCGCAAAGT 6240
 TGACTTGTCAAGTTTTTCTCGTCAATCTGGAAC TACTAAAGA TTTCTTAGCGGCTTTCA

Thr Glu Gln Leu Gln Lys Glu Gln Leu Asp Leu Asp Phe Leu Lys Asp Arg Glu Ser
 _____Yoml_____

AACAAACGGAAGAGAGCGCTCCAAGATCAGCTCGAAAAAGATGAGGAGTCAATCAACAAT 6300
 TTGTTTGCTTTCTTCGCGAGGTTCTAGTCGAGCTTTTCTACTCCTCAGTTAGTTGTTA

Asn Lys Arg Lys Glu Ala Leu Gln Asp Gln Leu Glu Lys Asp Glu Ser Ile Asn Asn
 _____Yoml_____

AAATACGATAATCTTGTAATGATGAACGAGCCCTTAAAAAGCTTGAGGATGAAGATTATG 6360
 TTTATGCTATTAGAACATTTACTACTTGCTCGGAAATTTTTCGAAC TCTTATCTAATAC

Lys Tyr Asp Asn Leu Val Asn Asp Glu Arg Ala Phe Lys Lys Leu Glu Asp Lys Ile Met
 _____Yoml_____

AATGGAAAAATCACCGATATCGCTAAGCAGCTTAATGAGTTTTTCTAAGTTTATTATAATACC 6420
 TTACCTTTTATAGTGGCTATAGCGATTTCGTCGAATTACTCAAAGATTCAAAATAATTATGG

Asn Gly Lys Ile Thr Asp Ile Ala Lys Gln Leu Asn Glu Phe Ser Lys Phe Ile Asn Thr
 _____Yoml_____

FIG._ 1N-1

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107180' E812E660

AATATGGAGTCCATTGGAAAAGTATTTCAAACAACCTGATTGATAAACTCAAAGAAGCA
 TTATACCTCAGSTAACCTTTTTCATAAAGTTGTTGGACTAACTATTGAGTTTCTTCGT
 6480

Asn Met Glu Ser Ile Gly Lys Ser Ile Ser Asn Asn Leu Ile Asp Lys Leu Lys Glu Ala
 Yomi

TCTAATGCACIGAACTACTGCTGTCACAAAGGCAACACGACAGGTAATAAAGTATCCTCTTTT
 AGATTACGTTGACTTATGACGACAGTTTCCGTTGTGCTGTCCATTTTTCATAGGAGAAAG
 6540

Ser Asn Ala Leu Asn Thr Ala Val Lys Gly Asn Thr Thr Gly Lys Lys Val Ser Ser Phe
 Yomi

GCTTCTGGAGGTACACISGAACACAGGATTAGGTGCTGGTAACCTTGCATTCTTACATGAC
 CGAAGACCTCCCATGTGACCTTGTCTTAATCCACGACCATTTGAACGTAAGGATGACTG
 6600

Ala Ser Gly Gly Tyr Thr Gly Thr Gly Leu Gly Ala Gly Lys Leu Ala Phe Leu His Asp
 Yomi

AAAGAACTGATCTTAAATAAACTGACACAGGCCAACATCTTGATACGGTAAAAAGCTGTT
 TTCTTGACTAGAAITTTATTTTGACTGTGTCGGTTGTAGGAACATATGCCATTTTCACAAA
 6660

Lys Glu Leu Ile Leu Asn Lys Thr Asp Thr Ala Asn Ile Leu Asp Thr Val Lys Ala Val
 Yomi

FIG. 1N-2

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107180' E812E660

CGTGAACCGCTGTGGACGATTCCCAAAATGGGCCAAGGAGTAAAAATTAGCAGACCTT
 GCACCTTGGCGACACCTGCTAAGGGGTTTACCCCGGTTCCCTCATTTTAATCGTCTGGAA
 6720

Arg Glu Thr Ala Val Asp Asp Ser Pro Lys Trp Gly Gln Gly Val Lys Leu Ala Asp Leu
 Yomi

ATTAAAAAGGAATTACTTCTATTCCCTTCATTAGTTCTAAGTTAATCAATCAATGTTA
 TAAITTTTTCCTTAATGAAGATAAGGAAGTAATCAAGGATTGCAATTAGTTAGTTACAA
 6780

Ile Lys Lys Gly Ile Thr Ser Ile Pro Ser Leu Val Pro Asn Val Asn Gln Ser Met Leu
 Yomi

ACAAACAGTTTAAATTCCAAATTTAAAGAAGATTGAGATCCCCICAAAAACAATTGCTTCT
 GTTTGTCAAATTAAGGTTAAATTTCTTCTAACTCTAGGGGAGTTTTTGTAAACGAAGA
 6840

Thr Asn Ser Leu Ile Pro Asn Leu Lys Lys Ile Glu Ile Pro Ser Lys Thr Ile Ala Ser
 Yomi

TCGGAGATAAAACAATTAATTTACGAATACTTTCCACATTGATAAGCTAATAGGAGA
 AGACCTCTATTTTGTAAATTAATTTGCTTATGAAAAGGTGTAACATTTCGATTATCCTCCT
 6900

Ser Gly Asp Lys Thr Ile Asn Leu Thr Asn Thr Phe His Ile Asp Lys Leu Ile Gly Gly
 Yomi

FIG._10-1

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102180-80128660

GAATCGGGAGCGAGATCGATGTTTGAAGCATTAAAAACGAAGTTGTAAACTAAATGGT 6960
 CTTAGCCCTCGGCTCTAGCTACAAACTTCGTAATTTTTCCTTCACATTTTGATTACCA

Glu Ser Gly Ala Arg Ser Met Phe Glu Ser Ile Lys Asn Glu Val Val Lys Leu Asn Gly
 —Yoml—

AGCATGTAGAGTCTGC AAAAGCAGACTCTTTATTTAACCTTGAGGTGGAACCTCA 7020
 TCGTACATTCTCAGACGTTTCGCTCGAGAAATAAATTGAATTGAACTCCACCTTTGAGT

Ser Met
 -Yoml—

TGATTAGAGAAGTCAATACTTTATGTTCATAATAATATCCCTTCTTATGAATTAGGAGCCG 7080
 ACTAATCTCTTCAGTTATGAAATACAAGTTATTATAGGGAAGAATACTTAATCCTCGGC

TAAATGTAAATACAGAAGGA
 —————→ 7100
 ATTACATTTATGTCCTCCT

FIG. 10-2

lasa_psea.pe	60	70	80	90	100	110
	PKVLLTLMWNQSGFLGAFDERALAAPLGRLSAKRGFD--AQVRDVLQOLSRRYVGEFVQL					
YOMI		:	:	:	:	:
	1400	1410	1420	1430	1440	1450
	IVTSTTSSGGTTSSTGSGYSKYSSYNSAAKYNVDPALIAAVIQES-----GFN----					
lasa_psea.pe	120	130	140	150	160	170
	RQAAARKAVCEQCLNA---ASAILGLLREGAKVSAVQGNPLGAVATQFQLRFTPAAE					
YOMI		:	:	:	:	:
	1460	1470	1480	1490	1500	
	--AKARSGVGAGMLQMLPATAKSLGVNNAYDPYQNVWGGTKY--LAQQLER-FCGNVEK					
lasa_psea.pe	180	190	200	210	220	
	LLQPSNRVARQLQAAALAPSNLMQLPWRQ---GYSMQGNAGHSNTGSGYPYSS-FDAS					
YOMI		:	:	:	:	:
	1510	1520	1530	1540	1550	1560
	ALAAYNAGCGNV-IKYGGIPPFKETQNYVKKIMANYSKLSUSSATSIASYYTNNSAFRVS					
lasa_psea.pe	230	23	240	250	260	270
	YDPRRWGSAITSV-----VAAHAGT-VRVLSRCQVRVTHPSGATNY--HMQIOQVSN					
YOMI		:	:	:	:	:
	1570	1580	1590	1600	1610	1620
	SKYGOQESGLASSPHKGTDFPAKAGATAIKSLQSGKVQIAGYSKTACGNVWVLIKQDDGTVAK					
lasa_psea.pe	280	290	300	310	320	330
	GOQV--SADTKLG--VTAGNINTALCEGSGSTGPHLHFLSYLYNGAEVSLQAGSEFYPIN					
YOMI		:	:	:	:	:
	1630	1640	1650	1660	1670	1680
	YMHMLTPSVKAGOSVKAGQGTICKGVSTGNSTGNHLLHQLJEONGKTI DPE-----KYNQG					
lasa_psea.pe	340	350	360	370		
	VGTSNVYDNCRRYVYFQNSAGTTHCAFRFLYNPLGAL					
YOMI		:	:	:	:	:
	1690	1700	1710	1720	1730	1740
	IGTISIDASQAEARQGTIAQAKSDLLLSLOGDISSVNDQTOIELQVELYVQSKLIDEFKRRIG					

FIG. 2